



#6/43

RECEIVED

JUN 26 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> MURDIN, ANDREW D.  
OOMEN, RAYMOND P.  
WANG, JOE  
DUNN, PAMELA

<120> CHLAMYDIA ANTIGENS AND CORRESPONDING  
DNA FRAGMENTS AND USES THEREOF

<130> 032931/0227

<140> 09/523,647

<141> 2000-03-10

<150> 60/123,966

<151> 1999-03-12

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2111

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (139)..(1809)

<400> 1

ttgatcagg agttaggaga tgaattaatt cctgactacc ttaattcaga taataaaaccc 60

aaatgttgag ggtaagagtt tacaaaacat tctacccgat ggcagaagaa aaaaataaac 120

atgcgatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc 171  
Met Ser Lys Leu Ile Arg Arg Val Val Thr Val  
1 5 10

ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag 219  
Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu  
15 20 25

gcc gct gta gca gag tct ctg att act aag atc gtc got agt gcg gaa 267  
Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu  
30 35 40

aca aag cca gca cct gtt cct atg aca gcg aag aag gtt aga ctt gtc 315  
Thr Lys Pro Ala Pro Val Pro Met Thr Ala Lys Lys Val Arg Leu Val  
45 50 55

cgt aga aat aaa caa cca gtt gaa caa aaa agc cgt ggt gct ttt tgt 363  
Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys  
60 65 70 75

gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag 411  
 Asp Lys Glu Phe Tyr Pro Cys Glu Gly Arg Cys Gln Pro Val Glu  
       80                 85                 90

gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac 459  
 Ala Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn  
       95                 100                 105

gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act 507  
 Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr  
       110                 115                 120

gta gga tct cct tac cct att gaa atc ctt gct ata ggc aaa aaa gat 555  
 Val Gly Ser Pro Tyr Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp  
       125                 130                 135

tgt gtt gat gtt gtg att aca caa cag cta cct tgc gaa gct gaa ttc 603  
 Cys Val Asp Val Val Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe  
       140                 145                 150                 155

gta agc agt gat cca gaa aca act cct aca agt gat ggg aaa tta gtc 651  
 Val Ser Ser Asp Pro Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val  
       160                 165                 170

tgg aaa atc gat cgc ctg ggt gca gga gat aaa tgc aaa att act gta 699  
 Trp Lys Ile Asp Arg Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val  
       175                 180                 185

tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttc aca gct gct act gta 747  
 Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val  
       190                 195                 200

tgt gct tgc cca gag ctc cgt tct tat act aaa tgc ggt caa cca gcc 795  
 Cys Ala Cys Pro Glu Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala  
       205                 210                 215

att tgt att aag caa gaa gga cct gac tgt gct tgc cta aga tgc cct 843  
 Ile Cys Ile Lys Gln Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro  
       220                 225                 230                 235

gta tgc tac aaa atc gaa gta gtg aac aca gga tct gct att gcc cgt 891  
 Val Cys Tyr Lys Ile Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg  
       240                 245                 250

aac gta act gta gat aat cct gtt ccc gat ggc tat tct cat gca tct 939  
 Asn Val Thr Val Asp Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser  
       255                 260                 265

ggt caa aga gtt ctc tct ttt aac tta gga gac atg aga cct ggc gat 987  
 Gly Gln Arg Val Leu Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp  
       270                 275                 280

aaa aag gta ttt aca gtt gag ttc tgc cct caa aga aga ggt caa atc 1035  
 Lys Lys Val Phe Thr Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile  
       285                 290                 295

act aac gtt gct act gta act tac tgc ggt gga cac aaa tgt tct gca Thr Asn Val Ala Thr Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala 300 305 310 315	1083
aat gta act aca gtt gtt aat gag cct tgt gta caa gta aat atc tct Asn Val Thr Thr Val Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser 320 325 330	1131
ggt gct gat tgg tct tac gta tgt aaa cct gtg gag tac tct atc tca Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser 335 340 345	1179
gta tcg aat cct gga gac ttg gtt ctt cat gat gtc gtg atc caa gat Val Ser Asn Pro Gly Asp Leu Val Leu His Asp Val Val Ile Gln Asp 350 355 360	1227
aca ctc cct tct ggt gtt aca gta ctc gaa gct cct ggt gga gag atc Thr Leu Pro Ser Gly Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile 365 370 375	1275
tgc tgt aat aaa gtt gtt tgg cgt att aaa gaa atg tgc cca gga gaa Cys Cys Asn Lys Val Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu 380 385 390 395	1323
acc ctc cag ttt aaa ctt gta gtg aaa gct caa gtt cct gga aga ttc Thr Leu Gln Phe Lys Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe 400 405 410	1371
aca aat caa gtt gca gta act agt gag tct aac tgc gga aca tgt aca Thr Asn Gln Val Ala Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr 415 420 425	1419
tct tgc gca gaa aca aca cat tgg aaa ggt ctt gca gct acc cat Ser Cys Ala Glu Thr Thr His Trp Lys Gly Leu Ala Ala Thr His 430 435 440	1467
atg tgc gta tta gac aca aat gat cct atc tgt gta gga gaa aat act Met Cys Val Leu Asp Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr 445 450 455	1515
gtc tat cgt atc tgt gta act aac cgt ggt tct gct gaa gat act aac Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn 460 465 470 475	1563
gta tct tta atc ttg aag ttc tca aaa gaa ctt cag cca ata gct tct Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser 480 485 490	1611
tca ggt cca act aaa gga acg att tca ggt aat acc gtt gtt ttc gac Ser Gly Pro Thr Lys Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp 495 500 505	1659
gct tta cct aaa ctc ggt tct aag gaa tct gta gag ttt tct gtt acc Ala Leu Pro Lys Leu Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr 510 515 520	1707

ttg aaa ggt att gct ccc gga gat gct cgc ggc gaa gct att ctt tct 1755  
 Leu Lys Gly Ile Ala Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser  
 525 530 535

tct gat aca ctg act tca cca gta tca gac aca gaa aat acc cac gtg 1803  
 Ser Asp Thr Leu Thr Ser Pro Val Ser Asp Thr Glu Asn Thr His Val  
 540 545 550 555

tat taa attctaagga attatcctaa agcagagcga tattccgctc tgcttttagga 1859  
 Tyr

tagcttcaa agaagtaccg cttagtacc ttacgtacta aagcggtttt tttgttttat 1919  
 aagctttca atccaatcgt agagttctt aatcaaagat attatthaag tttctgaaat 1979  
 cctaagattt attttaaaag cccatcttt taggtatgta attaaaattt ttaattaagc 2039  
 ttttcctagt gtaacctgct tcttagaa ctacactagg agaacggtat gtcataaat 2099  
 ctacatcccc ta 2111

<210> 2  
<211> 556  
<212> PRT  
<213> Chlamydia pneumoniae

<400> 2  
Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser  
 1 5 10 15

Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu  
 20 25 30

Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro  
 35 40 45

Val Pro Met Thr Ala Lys Lys Val Arg Leu Val Arg Arg Asn Lys Gln  
 50 55 60

Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys Asp Lys Glu Phe Tyr  
 65 70 75 80

Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser  
 85 90 95

Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val  
 100 105 110

Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr  
 115 120 125

Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val  
 130 135 140

Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro  
 145 150 155 160

Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg  
 165 170 175

Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu  
 180 185 190

Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu  
 195 200 205

Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala Ile Cys Ile Lys Gln  
 210 215 220

Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile  
 225 230 235 240

Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp  
 245 250 255

Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu  
 260 265 270

Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr  
 275 280 285

Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr  
 290 295 300

Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val  
 305 310 315 320

Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser  
 325 330 335

Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly  
 340 345 350

Asp Leu Val Leu His Asp Val Val Ile Gln Asp Thr Leu Pro Ser Gly  
 355 360 365

Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val  
 370 375 380

Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys  
 385 390 395 400

Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala  
 405 410 415

Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr  
 420 425 430

Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp  
 435 440 445

Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys  
 450 455 460

Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu  
465 470 475 480

Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys  
485 490 495

Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu  
500 505 510

Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala  
515 520 525

Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr  
530 535 540

Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr  
545 550 555

<210> 3  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 3  
ataagaatgc ggccgccacc atgtccaaac tcatcagacg agtag 45

<210> 4  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 4  
gcgcggatc cgatacacgt gggattttc tgtg 34